SI2-SSE: Plant genome alignment reveals mechanism of chromosome number reduction

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INTRODUCTION

We have been developing a novel multiple-genome alignment software toolkit, and using programs developed so far, we comparatively studied the genome structures of grass and Arabidopsis plants. Whole-genome duplication, or polyploidization, typically doubles chromosome numbers in one generation. After that, chromosome numbers usually decline, sometimes eventually restoring the pre-polyploidy number. Chromosome number reduction has largely resulted from chromosome fusion, and biological mechanisms by which this occurs have been discussed. However, previous inference about the proposed mechanisms is still coarse and incompletely explains this complex dynamic process. Our recent study let us show how chromosome numbers reduced after recursively doubling or tripling in polyploidization. With other lines of evidence from human and yeast, we propose a new theory, emphasizing upon telomere-centric mechanism, to explain chromosome number reduction during the evolution of eukaryotes, which have linear chromosomes.

RESULTS

- With the support of this project, we have developed multiple software elements to align and graphically show genome alignment from global to local levels.
- Based on gene colinearity, we have developed software to align 9 grasss genomes, which is essential to under grass genome evolution and functional innovation of genes.

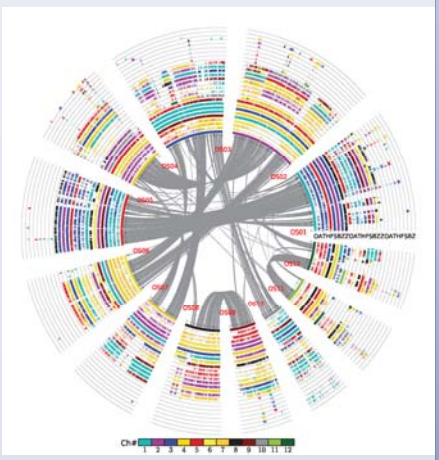


Figure 1. Alignment of grass Genomes. Genomes are aligned using rice as reference. The whole-genome duplication in the common ancestor of these grasses causes all to have at least two circles of chromosomes, and an additional lineage-specific whole-genome duplication causes maize to have four. Each species has another circle to contain additional duplicated regions. Genes are colored according to their corresponding rice chromosome. For example, genes from all grasses with orthologs on rice chromosome 1 are in blue. O: Oryza sativa; A: Aegilops tauschii(wheat D genome); T: Triticum urartu(wheat A genome); H: Hordeum vulgare L.(Barley genome); F: Foxtail millet; S: Sorghum bicolor; B: Brachypodium distachyon; Z: Zea mays.

- Homologous dotploting based gene homology is simple but of paramount importance to understand the genome structure evolution. Based on this, we found how chromosomes changed before and after speciation, and even compare the effectiveness of different softwares.

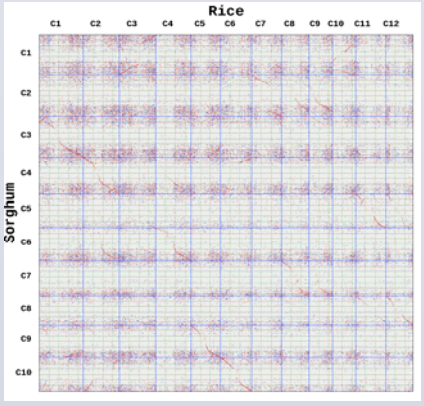


Figure 2. Homologous dotplot between rice and sorghum.

- By comparatively analysis grass genomes and Arabidopsis genomes, we revealed the mechanisms of karyotype evolution, and showed that chromosome number reduction was accompanied by the production of satellite chromosomes, formed by two telomeres from the same chromosome or two different chromosomes.

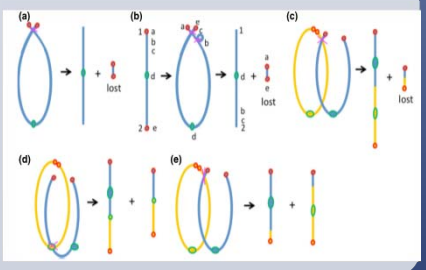
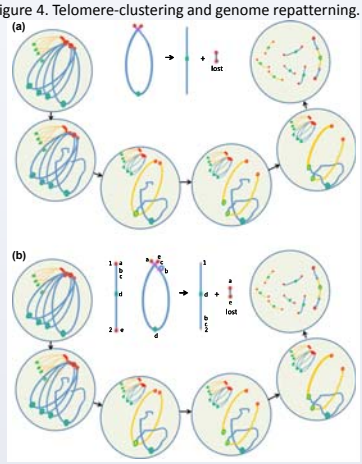


Figure 3. Telomere-centric genome repatterning. Blue or gold bars show chromosomes, red circles show telomeres, and green circles show centromeres. Crossover at telomere-proximal regions, within a chromosome or between different chromosomes may occur. Free-end chromosome may be produced following the formation of ring chromosome (a, b), and it may invade and insert into another chromosome (e). The production of satellite chromosomes results in chromosome number reduction.

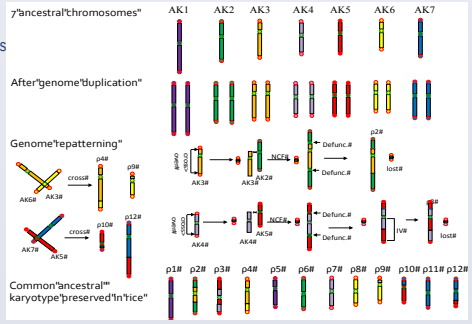
- During the process of chromosomal telomere clustering, cross-overs may happen, leading to genome repatterning. In Figure 4: a. A two-free-end chromosome produced in a process described in Fig. 2a may find a DNA region (often pericentromeric regions) to attach to, resulting in breakage of the affected chromosome. If one free end of the first chromosome is ligated with one broken end of the second chromosome, the two chromosomes would each have a remaining free end, and their proximity may increase the chance that they ligate. Therefore, the first chromosome merges into the second one and a large novel chromosome is formed; b. Similar to a, but the affected chromosome is the duplicated copy of the two-free-end chromosome.

Figure 4. Telomere-clustering and genome repatterning.



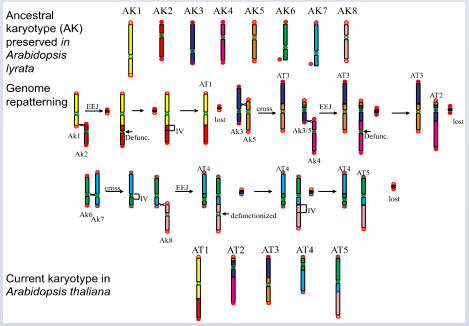
- In Figure 5, we showed the cell karyotype changes before and after whole-genome duplication in grass common ancestor, from diploid 2n = 14 chromosomes to 4n = 28 chromosomes, and after genome repatterning, eventually the grass common ancestor had 24 chromosomes, well preserved in the rice genome. In Figure 4, repatterning of some grasses are shown.

Figure 5. Ancestral grass genome repatterning.



- We also showed the cell karyotype changes to form A. thaliana genome.

Figure 6. Genome repatterning to produce *A. thaliana*.



CONCLUSIONS

- Chromosome number reduction is best explained by intra- and/or inter-chromosomal crossovers to form new chromosomes that utilize the existing telomeres of 'invaded' and centromeres of 'invading' chromosomes, the alternative centromeres and telomeres being lost.
- Comparison to the banana genome supports the grass common ancestor had 7 chromosomes rather than the 5 raised previously.
- The 'invading' and 'invaded' chromosomes are frequently homoeologs, originating from duplication of a common ancestral chromosome.
- Telomere-centric chromosome number reduction following recursive whole-genome duplication in plants is also important in mammals and yeast, and may be a general mechanism of restoring small linear chromosome numbers in higher eukaryotes.

REFERENCES AND CONTACT

- Wang X, et al. *New Phytologist*. 2015. (Published online in 2014).

- More figures and movies showing genome repatterning can be found at: http://onlinelibrary.wiley.com/.

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